RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:	10/05/345	
Source:	IFIDIG.	
Date Processed by STIC:	11-17-04	_

ENTERED



IFW16

RAW SEQUENCE LISTING DATE: 11/17/2004
PATENT APPLICATION: US/10/051,345 TIME: 09:48:29

Input Set : A:\PTO.LM.TXT

Output Set: N:\CRF4\11172004\J051345.raw

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3 <110 > APPLICANT: Fung, Yuen Kai
        Gomer, Charles
        Ang, Anne T'
 7 <120> TITLE OF INVENTION: Methods To Enhance And Confine Expression of Genes
 9 <130> FILE REFERENCE: D6087D
11 <140> CURRENT APPLICATION NUMBER: 10/051,345
12 <141> CURRENT FILING DATE: 2002-01-18
13 <150> PRIOR APPLICATION NUMBER: 60/096,947
14 <151> PRIOR FILING DATE: 1998-08-18
16 <160> NUMBER OF SEQ ID NOS: 9
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 441
20 <212> TYPE: DNA
21 <213> ORGANISM: Unknown .
23 <220> FEATURE:
25 <221> NAME/KEY: exon
26 <223> OTHER INFORMATION: sequence encoding N-terminus (amino acids 1-147)
        DNA-binding domain of yeast GAL4 protein
29 <400> SEQUENCE: 1
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30 atqaaqctac tgtcttctat cgaacaagca tgcgatattt gccgacttaa
31 aaageteaag tgeteeaaag aaaaaeegaa gtgegeeaag tgtetgaaga
                                                             100
                                                             150
32 acaactggga gtgtcgctac tctcccaaaa ccaaaaggtc tccgctgact
                                                             200
33 agggcacatc tgacagaagt ggaatcaagg ctagaaagac tggaacagct
34 atttctactg atttttcctc gagaagacct tgacatgatt ttgaaaatgg
                                                             250
35 attetttaca ggatataaaa gcattgttaa caggattatt tgtacaagat
                                                             300
36 aatgtgaata aagatgccgt cacagataga ttggcttcag tggagactga
                                                             350
                                                             400
37 tatqcctcta acattgagac agcatagaat aagtgcgaca tcatcatcgg
38 aagagagtag taacaaaggt caaagacagt tgactgtatc g
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41 <211> LENGTH: 315
42 <212> TYPE: DNA
43 <213> ORGANISM: Unknown
45 <220> FEATURE:
47 <221> NAME/KEY: exon
48 <223> OTHER INFORMATION: sequence encoding basic helix-loop-helix leucine
        zipper domain of Max (amino acids 8-112)
51 <400> SEQUENCE: 2
52 qaqqtqqaga qcqacqaaga qcaaccqaqq tttcaatctg cggctgacaa
                                                            50
53 acgggctcat cataatgcac tggaacgaaa acgtagggac cacatcaaag
54 acagetttea eagtttgegg gaeteagtee cateacteea aggagagaag
                                                            200
55 gcatcccggg cccaaatcct agacaaagcc acagagtata tccagtatat
56 gcgaaggaaa aaccacacac accaqcaaga tattgacgac ctcaagcggc
57 agaatgctct tctggagcag caagtccgtg cactggagaa ggcgaggtca
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58 agtgcccaac tgcag 315 60 <210> SEO ID NO: 3 61 <211> LENGTH: 33 62 <212> TYPE: DNA 63 <213> ORGANISM: Unknown 65 <220> FEATURE: 67 <221> NAME/KEY: exon 68 <223> OTHER INFORMATION: sequence encoding the first 11 amino acids of Gal4 70 <400> SEQUENCE: 3 71 atgaagctac tgtcttctat cgaacaagca tgc 73 <210> SEQ ID NO: 4 74 <211> LENGTH: 387 75 <212> TYPE: DNA 76 <213> ORGANISM: Unknown 78 <220> FEATURE: 80 <221> NAME/KEY: exon 81 <223> OTHER INFORMATION: sequence encoding the C-terminus transactivation domain of herpes simplex viral protein VP16 84 <400> SEQUENCE: 4 85 gcgtacagcc gcgcgcgtac gaaaaacaat tacgggtcta ccatcgaggg 50 86 cctgctcgat ctcccggacg acgacgcccc cgaagaggcg gggctggcgg 87 ctccqcqcct qtcctttctc cccqcqqqac acacqcqcaq actqtcqacq 88 gccccccga ccgatgtcag cctgggggac gagctccact tagacggcga 89 ggacgtggcg atggcgcatg ccgacgcgct agacgatttc gatctggaca 90 tgttggggga cggggattcc ccgggtccgg gatttacccc ccacgactcc 300 91 gccccctacg gcgctctgga tatggccgac ttcgagtttg agcagatgtt 92 taccgatgcc cttggaattg acgagtacgg tgggtag 94 <210> SEQ ID NO: 5 95 <211> LENGTH: 270 96 <212> TYPE: DNA 97 <213> ORGANISM: Unknown 99 <220> FEATURE: 101 <221> NAME/KEY: exon 102 <223> OTHER INFORMATION: sequence encoding the basic helix-loop-helix 103 leucine zipper domain of c-Myc 105 <400> SEQUENCE: 5 106 accgaggaga atqtcaagag gcgaacacac aacgtcttgg agcqccagag 107 gaggaacgag ctaaaacgga gettttttgc cetgegtgae cagateeegg 108 agttggaaaa caatqaaaag gcccccaagg tagttatcct taaaaaagcc 150 109 acagcataca teetqteeqt ecaaqcaqaq qaqcaaaaqc teatttetqa 200 110 agaggacttg ttgcggaaac gacgagaaca gttgaaacac aaacttgaac 250 111 agctacggaa ctcttgtgcg 270 113 <210> SEQ ID NO: 6 114 <211> LENGTH: 17 115 <212> TYPE: DNA 116 <213> ORGANISM: Unknown 118 <220> FEATURE: 120 <221> NAME/KEY: protein_bind 121 <223> OTHER INFORMATION: a 17-mer DNA-binding site for Gal4

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123 <400> SEQUENCE: 6
124 cggaggactg tcctccq
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126 <210> SEQ ID NO: 7
127 <211> LENGTH: 1008
128 <212> TYPE: DNA
129 <213> ORGANISM: Unknown
131 <220> FEATURE:
133 <221> NAME/KEY: misc_feature
134 <223> OTHER INFORMATION: TET-ON sequence
136 <400> SEQUENCE: 7
137 atgtctagat tagataaaag taaagtgatt aacagcgcat tagagctgct
138 taatgaggtc ggaatcgaag gtttaacaac ccgtaaactc gcccagaagc
139 ttggtgtaga gcagcctaca ctgtattggc atgtaaaaaa taagcgggct
                                                             150
140 ttgctcgacg ccttagccat tgagatgtta gataggcacc atactcactt
141 ttgcccttta aaaggggaaa gctggcaaga ttttttacgc aataacqcta
142 aaagttttag atgtgcttta ctaagtcatc gcaatggagc aaaagtacat
143 tcagatacac ggcctacaga aaaacagtat gaaactctcg aaaatcaatt
                                                             350
144 agccttttta tgccaacaag gtttttcact agagaacgcg ttatatgcac
                                                             400
145 teagegetgt ggggeatttt actttaggtt gegtattgga agateaagag
146 catcaagtcg ctaaagaaga aagggaaaca cctactactg atagtatgcc
147 gccattatta cgacaagcta tcgaattatt tgatcaccaa ggtgcaqaqc
148 cagcettett atteggeett gaattgatea tatgeggatt agaaaaacaa
149 cttaaatgtg aaagtgggtc cgcgtacagc cgcgcgcgta cgaaaaacaa
150 ttacgggtct accatcgagg gcctgctcga tctcccggac gacgacgccc
                                                             700
151 ccgaagaggc ggggctggcg gctccgcgcc tgtcctttct ccccqcqqqa
152 cacacgegea gaetgtegae ggeeeeeeeg acegatgtea geetgqqqqa
153 cgagetecae ttagaeggeg aggaegtgge gatggegeat geegaegege
                                                             850
154 tagacgattt cgatctggac atgttggggg acggggattc cccgggtccg
                                                             900
155 ggatttaccc cccacgactc cgccccctac ggcgctctgg atatggccga
                                                            950
156 cttcgagttt gagcagatgt ttaccgatgc ccttggaatt gacgagtacg 1000
157 gtgggtag
                                                             1008
159 <210> SEQ ID NO: 8
160 <211> LENGTH: 80
161 <212> TYPE: DNA
162 <213> ORGANISM: Unknown
164 <220> FEATURE:
166 <221> NAME/KEY: misc feature
167 <223> OTHER INFORMATION: the first 80 bases of TET-ON sequence
169 <400> SEQUENCE: 8
170 atgtctagat tagataaaag taaagtgatt aacagcgcat tagagctgct
171 taatgaggtc ggaatcgaaq qtttaacaac
173 <210> SEQ ID NO: 9
174 <211> LENGTH: 621
175 <212> TYPE: DNA
176 <213> ORGANISM: Unknown
178 <220> FEATURE:
180 <221> NAME/KEY: exon
181 <223> OTHER INFORMATION: sequence encoding tet repressor (amino acids 1-207)
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183 <400> SEQUENCE: 9

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184	atgtctagat	tagataaaag	taaagtgatt	aacagcgcat	tagagctgct	50
185	taatgaggtc	ggaatcgaag	gtttaacaac	ccgtaaactc	gcccagaagc	100
186	ttggtgtaga	gcagcctaca	ctgtattggc	atgtaaaaaa	taagcgggct	150
187	ttgctcgacg	ccttagccat	tgagatgtta	gataggcacc	atactcactt	200
		aaaggggaaa				250
189	aaagttttag	atgtgcttta	ctaagtcatc	gcaatggagc	aaaagtacat	300
190	tcagatacac	ggcctacaga	aaaacagtat	gaaactctcg	aaaatcaatt	350
191	agccttttta	tgccaacaag	gtttttcact	agagaacgcg	ttatatgcac	400
192	tcagcgctgt	ggggcatttt	actttaggtt	gcgtattgga	agatcaagag	450
193	catcaagtcg	ctaaagaaga	aagggaaaca	cctactactg	atagtatgcc	500
		cgacaagcta				550
		attcggcctt				600
196	cttaaatgtg	aaagtgggtc	C			621

VERIFICATION SUMMARY

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